# IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

)
) FOR: METHOD FOR PREDICTING ) PROTEIN-PROTEIN ) INTERACTIONS IN ENTIRE
) PROTEOMES
) Group ) Art Unit: Uknown
ARY AMENDMENT
ion of this application, please enter the
I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231 on:
November 14, 2001 (Mailing Date)
Melissa J. Leffler (Typed Name)
(Signature)  November 14, 2001  (Date of Signature)

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### IN THE TITLE

Please amend the title to read:

Method for Predicting Protein Binding from Primary Structure Data.

#### **REMARKS**

The Applicants inadvertently entered the incorrect title in the Oath and Declaration and the Assignment documents. The error was not noted until after the documents were signed. Please change the title of the application to read as listed above. The Applicants certify that this change does not constitute new matter.

Respectfully submitted,

Dated: November 14, 2001

By:

Colleen J. McKiernan Attorney for Applicant Registration No. 48,570

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Docket No.: 6627-PA1034

### INDICATION OF CHANGES MADE IN THE TITLE

METHOD FOR PREDICTING PROTEIN(-PROTEIN INTERACTIONS IN ENTIRE PROTEOMES) BINDING DATA FROM PRIMARY STRUCTURE DATA

# METHOD FOR PREDICTING PROTEIN BINDING FROM PRIMARY STRUCTURE DATA

## **CROSS-REFERENCES TO RELATED APPLICATIONS**

[0001] This application claims the benefit of priority of United States provisional application Serial Number 60/248,258 filed November 14, 2001 which is incorporated herein by reference in its entirety.

### **COMPUTER APPENDIX**

[0002] A computer program listing appendix submitted in duplicate on compact disc under § 1.52 ((e) 5) with the application is hereby incorporated by reference.

### FIELD OF THE INVENTION

[0003] The invention is a trainable system and computational method for predicting the interaction of biopolymers with other biopolymers, nucleic acids, and with a variety of ligands based on the sequence or primary structure of the biomolecule.

## **BACKGROUND OF THE INVENTION**

[0004] Determination of protein-protein interaction is a slow and cumbersome process. Methods such as the yeast two-hybrid system can reveal unexpected, transient protein-protein interactions in cells. Alternatively, more stable protein-protein interactions may be determined by immunoprecipitations and other *in vitro* binding assays. However, it is generally not possible to determine the specific sites of interaction between the proteins by these methods. High-resolution structural analysis can reveal protein-protein interactions at a molecular level. Structures can be obtained for protein complexes, but only proteins already known to interact would be studied in this manner. Pairs of proteins may be studied individually to predict protein-protein